change "approx" to -- about --

IN THE CLAIMS

Please cancel claims 11 to 13, 16 to 22, 28 to 39, 41 and 42 without prejudice, add new claims 86 to 91, and amend the claims as indicated below.

Upon entry of the present amendment, the status of the claims will be as follows:

1. (currently amended) A method for detecting ~~a hepatic cell proliferative disorder~~ liver cancer in a human, comprising: detecting hypermethylation of a ~~methylated~~ CpG-containing promoter region at approximately nucleotide positions -539 to -239 or -195 to +35 of a glutathione-S-transferase P1 (GSTP1) gene transcription start site ~~(GST) nucleic acid~~ in a sample comprising nucleic acids from a hepatic tissue specimen, bile, or blood, ~~or biological fluid~~ wherein a ~~methylated GST nucleic acid~~ hypermethylation of the CpG-containing promoter region ~~from the transcription start site~~ is indicative of liver cancer ~~a hepatic cell proliferative disorder~~.

2. (currently amended) The method of claim 1, wherein the ~~GST nucleic acid~~ hypermethylation of the promoter region is detected by contacting the nucleic ~~acid~~ acids with ~~nucleic acid~~ GSTP1 oligonucleotide primers.

3. (currently amended) The method of claim 2, wherein the primers flank ~~a region in the promoter of GST~~ the promoter region at approximately nucleotide positions -195 to +35 of the GSTP1 gene~~, wherein said promoter contains a transcriptional start site for GST~~.

4. (currently amended) The method of claim 2, wherein the primers flank the promoter region ~~is~~ at approximately nucleotide positions -539 to -239 ~~upstream from the transcriptional start site~~ of the GSTP1 gene.

5. (original) The method of claim 2, wherein the nucleic acid primers are selected from the group consisting of SEQ ID NO:1, 2, 7, 8, 9, 10, 11, 12, 13, and combinations thereof.

6. (currently amended) The method of claim 1, wherein the detecting comprises contacting ~~a nucleic acid-containing hepatic specimen or biological fluid~~ the nucleic acids with an agent that modifies ~~unmethylated~~ nonmethylated cytosine residues, amplifying ~~the~~ CpG-containing nucleic acids ~~acid in the specimen~~ by means of CpG-specific oligonucleotide primers, wherein the oligonucleotide primers distinguish between modified methylated and nonmethylated nucleic acid, and detecting the methylated CpG-containing promoter region ~~GST nucleic acid~~ based on the presence or absence of amplification products produced in said amplifying step.

7. (currently amended) The method of claim 6, wherein the amplifying step ~~is the~~ comprises a polymerase chain reaction ~~(PCR)~~.

8. (previously amended) The method of claim 6, wherein the oligonucleotide primers have a sequence selected from the group consisting of SEQ ID NO: 7, 8, 9, 10, 11, 12, and 13.

9. (original) The method of claim 6, wherein the modifying agent is bisulfite.

10. (original) The method of claim 6, wherein cytosine is modified to uracil.

11 to 13. (cancelled)

14. (currently amended) The method of claim ~~6~~ 1, ~~further comprising contacting the nucleic acid~~ wherein the detecting comprises contacting the nucleic acids or a GSTP1 amplification product thereof with a methylation sensitive restriction endonuclease.

15. (original) The method of claim 14, wherein the restriction endonuclease is selected from the group consisting of *MspI*, *HpaII*, *BssHII*, *BstUI* and *NotI*.

16 to 22. (cancelled)

23. (currently amended) The method of claim ~~16~~ 1, wherein the ~~reagent is a~~ hypermethylation is detected by contacting the nucleic acids of the sample or a GSTP1 amplification product thereof, with a nucleic acid probe.

24. (original) The method of claim 23, wherein the probe is detectably labeled.

25. (original) The method of claim 24, wherein the label is selected from the group consisting of a radioisotope, a bioluminescent compound, a chemiluminescent compound, a fluorescent compound, a metal chelate, and an enzyme.

26. (original) The method of claim 1, further comprising detecting the presence of hepatitis B virus or hepatitis C virus.

27. (currently amended) The method of claim 1, ~~further comprising~~ wherein hypermethylation is detected by comparing the methylation status of the ~~GST nucleic acid~~ promoter region at approximately nucleotide positions –539 to –239 or –195 to +35 of the GSTP1 gene to the methylation status of the ~~GST nucleic acid~~ promoter region in adjacent normal hepatic tissue.

28 to 39. (cancelled)

40. (currently amended) A method for detecting ~~a hepatic cell proliferative disorder associated with a glutathione S-transferase (GST) nucleic acid in a subject~~ liver cancer in a human, comprising contacting a target cellular component containing a ~~GST~~ nucleic acid with a reagent which reacts with ~~the GST nucleic acid~~ a CpG-containing promoter region at approximately nucleotide positions -539 to -239 or -195 to +35 of a glutathione-S-transferase P1 (GSTP1) gene transcription start site and detecting hypermethylation of the ~~GST nucleic acid~~ CpG-containing

promoter region, wherein hypermethylation of the ~~GST nucleic acid~~ promoter region is indicative of liver cancer ~~a hepatic cell proliferative disorder~~.

41 and 42. (canceled)

43. (original) The method of claim 40, wherein the reagent is a probe.

44. (currently amended) The method of claim 43, wherein the probe is ~~a nucleic acid~~ an oligonucleotide probe.

45. (original) The method of claim 43, wherein the probe is detectably labeled.

46. (original) The method of claim 45, wherein the label is selected from the group consisting of a radioisotope, a bioluminescent compound, a chemiluminescent compound, a fluorescent compound, a metal chelate, or an enzyme.

47. (original) The method of claim 40, wherein the reagent is a restriction endonuclease.

48. (original) The method of claim 47, wherein the restriction endonuclease is methylation sensitive.

49. (original) The method of claim 48, wherein the restriction endonuclease is selected from the group consisting of *MspI*, *HpaII*, *BssHII*, *BstUI* and *NotI*.

50. (previously amended) The method of claim 40, further comprising detecting the presence of hepatitis B virus or hepatitis C virus.

51. (previously amended) The method of claim 40, further comprising comparing the methylation status of the GST nucleic acid to the methylation status of the GST nucleic acid in adjacent normal hepatic tissue.

52 to 75. (cancelled)

~~76 to 83. (withdrawn)~~ Cancel

84. (currently amended) The method of claim 1 or claim 40 ~~as in any of claims 1, 28, or 40~~, wherein methylation is in one allele.

85. (currently amended) The method of claim 1 or claim 40 ~~as in any of claims 1, 28, or 40~~, wherein methylation is in both alleles.

86. (new) The method of claim 1, wherein the liver cancer is hepatocellular carcinoma.

87. (new) The method of claim 40, wherein the liver cancer is hepatocellular carcinoma.

88. (new) The method of claim 1, wherein the CpG-containing promoter region is at approximately nucleotide positions -80 and +35 of the GSTP1 gene transcriptional start site.

89. (new) The method of claim 40, wherein the CpG-containing promoter region is at approximately nucleotide positions -80 and +35 of the GSTP1 gene transcriptional start site.

90. (new) The method of claim 1, wherein the CpG-containing promoter region is at approximately nucleotide positions -343 and -301 bp from the GSTP1 gene transcription start site.

91. (new) The method of claim 40, wherein the CpG-containing promoter region is at approximately nucleotide positions -343 and -301 bp from the GSTP1 gene transcription start site.